



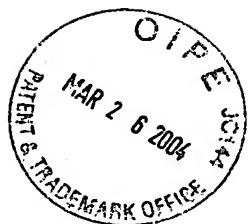
10	20	30	40	50
ATGAATAACA	CATCTTGCAA	CTTCAACGTC	ACTCTCAACG	CATCGGCACC
60	70	80	90	100
AAGCCGATAC	ATAGCTATTG	CTATGTACAG	CATTGTTATC	TGTATCGGGT
110	120	130	140	150
TGGTTGGAAA	CCTGCTGTTA	TGCATCGTGT	TAGTCAAGAA	ACGCAAAC TG
160	170	180	190	200
CGATATTCCA	GCGATGTTTA	TTTTTTCCAC	GCCTCTATGG	CCGACCTCGT
210	220	230	240	250
CAGCACTGTC	ATGCTACCGC	TCTGGCTACA	TTATGTCCTC	AACTTTGCCC
260	270	280	290	300
AACTCTCTCG	AGGAGCCTGT	ATCAGCTTTT	CGGTGACTTT	CTATGTTCCC
310	320	330	340	350
CTTTTCGTTC	AGGCCTGGTT	ACTCATTTCC	ATCGCTATGG	AGCGATATTC
360	370	380	390	400
CAACTTAGTA	TGGATGGCAC	CCATTAGCGT	TAAGACGGCC	TTTAAACACT
410	420	430	440	450
GCATAGGAAC	CTGGATCGTA	TCTGCCTTCG	TGGCATCACC	CTACTACGCA
460	470	480	490	500
TACAGAAACT	CACACGACGA	ACACGAATGC	ATTCTAGGAA	ACTACACTTG
510	520	530	540	550
GCACATTAAC	GAACCGCTAC	ACACGTGTAT	GGATGTGGTG	ATCATAGTAT
560	570	580	590	600
GGACCTTTTT	GGCCCCAGTA	CTGGTAACCA	TTATAGCAAG	CGTCAAAATG
610	620	630	640	650
AGACGAACGA	CCTGGGGCAA	TACTAGGTTA	AACGAAAAGA	ACAGCGACAT
660	670	680	690	700
TCTTATAGTA	CTAGTTGTCA	TGACAGTGTT	CTTTTGGGGA	CCGTTTAATA
710	720	730	740	750
TCGTGTTGGT	TATTGACAAT	ATTTTACAGA	GATACTATGA	TACCACGAAT
760	770	780	790	800
TGCGATGTAG	AAAAGATTAA	ACATATCATG	GCTATGATCT	CAGAAGCCAT
810	820	830	840	850
TGTTTATTTT	CGCGGTATTA	CAGCACCTAT	TATTTATGTA	GGGATTAGTG
860	870	880	890	900
GCAGATTTCTG	CGAAGAGATT	TACTCTCTGT	TTAGACGCCA	GCCGTATAAC
910	920	930	940	950
GATTTGGACC	CCGATGCCAA	TCAATTTCATG	ATTGAACTCA	CTAGCCAGGG
960	970	980	990	1000
AAGAAGTAGA	AATAGAAATG	CTAGACAATC	GGAAAGCAAT	GTACCGCAAC
1010	1020			
CAGAAGAATG	CTTCTGGTAA			

FIG. 1



10	20	30	40	50
ATGACCAACG	CCGGACACTG	TCACATAAAC	GAAAGTCTCG	CGTCGTATGG
60	70	80	90	100
AATCGCTCCC	GCAGCTACCA	TTACCTTATA	CAGCATTGCG	GGAATCTGCG
110	120	130	140	150
GTGTCACGGG	AAATCTGTTA	ATACTTTTGG	TTTTGTTCAC	GAGACGCATA
160	170	180	190	200
CACTGGTTTCG	CAAATGACAT	CTACTATCTC	AACATGATCT	TTACAGACTT
210	220	230	240	250
TCTTGTTTTTC	ATTACATTAC	CCGCCTGGGT	TTACTACCTG	CTGAATTACA
260	270	280	290	300
CACAACTCTC	ACACTATGCC	TGCATTGCTC	TATCATTTGT	TTTTTACGTT
310	320	330	340	350
TCCATTTTTTA	TTCAAGCTGA	CTTTATGGTA	GCAGTGGCTA	TCGAGCGTTA
360	370	380	390	400
TCGAAGCCTA	GTGAAAAACA	AACCCCTTAG	CGTAAAAAAA	GCCAGCGTCA
410	420	430	440	450
GCTGCGCGTG	CATCTGGATC	ATTGTTATTA	TAGTGTCTTC	ACCATACTAC
460	470	480	490	500
ATGTTTAGAT	CGCAACACGA	AACAAATTCT	TGCATTCTAG	GAAACTACAC
510	520	530	540	550
CTGGCATATG	AACAGTCCTT	TTCGCACCAC	AATGGACGCA	TCCATTAAACA
560	570	580	590	600
TTTGGTCTTT	TGTCGTTCGG	GCCGTGACGA	CCTTGTTAAT	AGCCAGACGA
610	620	630	640	650
ATTTATGTAT	GTACTIONCAGG	CAACAAAAAA	ATGAACGCCA	GAGCCAGTGG
660	670	680	690	700
TTTGTTAGAG	GCCATGGTGA	TTAGCATGTT	ATTCTTCGGA	GGACTTTTCA
710	720	730	740	750
ACCTGAACAT	CTTTCGAGAC	ATAGTTTCGG	ACACATCGGA	AGACAATAAA
760	770	780	790	800
GACTGCACAT	ATCTTAAGCA	GGAACACTTT	ATTCGCATGG	TCGGTGTGGC
810	820	830	840	850
CCTCGTTTAC	GGGCGCGCTA	TATTCAACCC	TTTTATGTAT	ATGTGTGTGA
860	870	880	890	900
GTACCAGATT	GCGCCAAGAA	ATAAAATGTT	TGTTTATGCG	AATACCTTAT
910	920	930	940	950
GAAACACTAG	ATGCAGAACA	CGCTAAACTC	ATGGTTAATT	TAAAAAACAG
960	970	980	990	1000
AAATGCTAAT	GTACCCGATC	CTAAACCTCG	TGAATATGAA	TCTGTGTAT
1010				
AG-----				

FIG. 2



10 ATGACCAACA	20 CTAACAATAC	30 GACTTGTCAT	40 CTCAACGGAA	50 CTTTCGAAAC
60 TTTTAAAATC	70 ACCCGTCCAG	80 TAGCCATCAG	90 CGCCTACACT	100 GTACTCGTGG
110 TTATCGGACT	120 TTTGGGAAAC	130 ATTGTGCTGC	140 TCAGCGTGCT	150 CGTCGTGAAA
160 CGCAAGCTCA	170 AGTTTCCGAA	180 TGACATTTAC	190 TTTTTCAACG	200 CGTCTTTGGC
210 AGACGTTTTT	220 GCCGTCTGCA	230 TGTTGCCCGC	240 CTGGGTAAAC	250 TATGCACTGG
260 ACTCCACACA	270 ACTTAGCAAG	280 TTCTCATGTA	290 TCACTTTTAC	300 GTTTGGTTTT
310 TACGTCTCCC	320 TGTTTCATCCA	330 GGCCTGGATG	340 CTCATTCTGG	350 TCACCCTGGA
360 GCGATACGGA	370 TCTCTAGTCT	380 GGATCGCCCC	390 GATCACCAGA	400 AACAAAGCCA
410 TAGCGAATTG	420 TGTA CTCTTT	430 TGGCTTGTTT	440 CCATCTTCTT	450 GGCCGCACCT
460 TACTACTCTT	470 TTAGAAACGA	480 AAGCAACGAA	490 CACCAATGCA	500 TCATGAGAAA
510 CTATACCTGG	520 AGCGTTGGTG	530 AAACATGGCA	540 CATAGCCCTG	550 GATTTCTTAA
560 TTACGCTCAT	570 TACATTTATC	580 ATGCCAGTGA	590 CTATTGTGTT	600 AGCTCTGAGT
610 TTCAAAATGG	620 CCAGATGGTC	630 AACCTTTGGT	640 TACAGAAACC	650 TCACCAGCAG
660 AACCAGTCTT	670 ATCCTTATTT	680 TGATACTGAC	690 AGTAGCAGCA	700 GGGTTCTGGG
710 GACCTTTTCA	720 CCTATTTATG	730 TTTATAGAAA	740 ACGTGGCAGG	750 GCAGATTTAC
760 CACATTCAAA	770 AGGATTGCTG	780 GTACTTACAG	790 CTCAGACACT	800 TGTGTAGCTT
810 GATGACCGAA	820 ACCCTAGTGT	830 TTCTACGTTC	840 AGTTTTTAAC	850 CCTTATATTT
860 ATATGATAAT	870 CAGTTACAAG	880 TTTAGGCAGC	890 AGGTGCGCAG	900 TCTACTCAAG
910 CGTACTCAGT	920 ATGATGCTTT	930 GGACACGACT	940 CAGTTAGCAG	950 AAACTATGCA
960 GCTGAAAGCG	970 AAAGGTGTGC	980 CGGTGTCCGA	990 CCCCGCGCCG	1000 CATGACTGCG
1010 AATGCTTTTT	1020 GTAA-----			

FIG. 3



10	20	30	40	50
ATGAATTCGA	GCCAGCACAA	CATAAGCGTG	TTTCTCTCCA	TTGGAGCAGG
60	70	80	90	100
CCCCGTCATT	ACCGGATACA	CGTGCGTTTT	TCTGTTCTGGG	ATTCTGGGAC
110	120	130	140	150
ACTTTTACTT	GTATTGGAAA	AACCATCAGA	GACGACACCG	GACAAACAGT
160	170	180	190	200
TTCAGTGATG	TTTTATTTTCG	ACATCTCATG	ATCACCGAAG	AGGTCTTTAC
210	220	230	240	250
CCTCACCAT	CCCGTCTGGG	CGTATCACTT	AACTACTCAC	GGCAACTTAC
260	270	280	290	300
CGGGCTCGTG	GTGCCGAAGT	CTCACCTTCG	TTTTTTATCT	AACGGTATTC
310	320	330	340	350
GCTCGTGCCT	TCTTTTACCT	GCTCCTCATC	TGGGACCGAT	ACAGCGTAAT
360	370	380	390	400
CATCTGCAGA	CACCCTCTCC	CCGTTAATCT	GAACTACAGT	CAGGTCATAG
410	420	430	440	450
GCCTGTCTGT	CTGGCTGGTT	GCCGTACTGT	CAGCATCACC	GTTCTCCATT
460	470	480	490	500
TTTAACGGAA	GTGTGAAACA	ATGCCTGGGC	AACATGGGCA	GCATACCCAG
510	520	530	540	550
CGAATCGTCT	GCCGTTCTTA	ACCTGGAAGT	GCACCTGTGC	TCCTTCTGGT
560	570	580	590	600
TACCGCTCAT	CATGTCGGCT	AACTGTTACT	ACCAAGCAAA	ACGCCGAGCA
610	620	630	640	650
TCGCCTGACC	AACTCCACGA	ACTTTACCGA	TGCAGTTTGC	TAATTACCATA
660	670	680	690	700
TTCACAAC	TACGCTATCG	TATGGTTTCC	TTTCCATCTC	GCTTTACTCA
710	720	730	740	750
TAGACGCCCT	GATTAGCATA	AGCCATGTAG	AACCCTCTAG	CGCTCTCCAC
760	770	780	790	800
TGGGCATCCA	TTGTCGTTAC	CTGTAAATCA	TTTACATTTG	TATATGCGGG
810	820	830	840	850
CATAAGCCCA	CTAGTGTATT	TCACATGCTG	CCCCACCGTA	CGTCGCGAAC
860	870	880	890	900
TGCTGATGTC	TCTACGTCCA	TTCTTCACCT	GGATTTCCAG	CAAAACGCGG
910	920	930	940	950
CGAGGCTACG	CTCCGATTAA	AACACAACCT	TTAAACATCC	CCGACGAGCC
960	970	980	990	
GATAGATAAC	AAGTCACCGC	ACCTGTTAAA	CGAATAA---	

FIG. 4



Replacement Sheet

10	20	30	40	50
ATGACTACCA	CCACAATGAG	TGCTACCACG	AATTCCAGTA	CCACGCCTCA
60	70	80	90	100
AGCAAGCAGC	ACCACGATGA	CAACGAAGAC	AAGCACTCCT	GGCAATACAA
110	120	130	140	150
CTACTGGCAC	TACGTCCACC	CTGACAACGA	TATCAACAAC	TTCTAATGCT
160	170	180	190	200
ACCAGCATAA	CGTCTAATTT	AAGCACTACC	GGAAACCAA	CTGCAACTAC
210	220	230	240	250
CAATGCTACT	ACCTTCAGTT	CCACATTAAC	AACATCTACA	AATATAAGCA
260	270	280	290	300
GTACATTTTC	GACAGTTTCT	ACCGTCGCAT	CCAATGCAAC	ATGTAATTCT
310	320	330	340	350
ACAATCACAA	CGAATATTAC	AACTGCTTTT	ACTACAGCAG	CAAACACTAC
360	370	380	390	400
CGCAAGCAGC	CTCACCAGCA	TCGTAAC TTC	ACTTGCCACT	ACCATTGAAA
410	420	430	440	450
CCACATCATT	TGATTATGAT	GAGTCAGCAG	AAGCTTGCAA	CTTAACAGAC
460	470	480	490	500
ATCGTTCATA	CTACTAGATC	AGTGACAGTT	ACTTTCTATA	CTATCATATT
510	520	530	540	550
CATACTCGGC	CTTTTG GGAA	ACTTTCTGGT	TCTTATGACC	ATCATTTGGA
560	570	580	590	600
ACCGTCGCAT	TTCCTTTATG	GTTGAAATAT	ATTTCTGTAA	TCTAGCAATC
610	620	630	640	650
TCCGATCTTA	TGTTTGTATG	TACTTTACCA	TTTTGGATAA	TGTATCTTCT
660	670	680	690	700
TGAGCACGAC	GTCATGTCAC	ATGCATCCTG	TGTAGCAATG	ACAGCCATTT
710	720	730	740	750
TTTATTGCGC	GCTGTTTGCC	AGCACTGTTT	TCCTCTTGCT	AATTGTTTTA
760	770	780	790	800
GACAGATGTT	ACGCTATTCT	ATTAGGTACA	GAAAAAGCAA	ATAGACGTTT
810	820	830	840	850
ATTGCGCAAT	GCTGTTTCTG	GATGCATGCT	CATGTGGGGA	TTGTGTTTCA
860	870	880	890	900
TTTTAGCATT	ACCTCATTTT	ATCTTTATGA	AGAAAGGAAC	CAACGTATGT
910	920	930	940	950
GTAGCAGAGT	ATGAACCAGG	ACTTAACAAT	TTCTATGTTA	TTTTTATCAA
960	970	980	990	1000
TACTGAGGTG	AACCTATGCA	CCCTAGTTTT	GCCAGCCGCA	GCCATTATCT

FIG. 5A



1010 ACTGGTATCT	1020 TAAACTAACC	1030 AAAGCACTCA	1040 AAACCCATGA	1050 ACGACTGCGT
1060 CATAGGCTAA	1070 CGTCTCTAAA	1080 CATAGTGTTA	1090 GCTGTTGTCA	1100 TTGTATTTGC
1110 TTTGTTTTGG	1120 CTGCCGTATA	1130 ATCTCATGCT	1140 TATGATGTAT	1150 AGCTTAGTTC
1160 ACATGCAGAT	1170 ACCTTGGGAA	1180 TGCAGCTCTG	1190 AAAAAATACT	1200 GAGACGAAGT
1210 TTAATTATTA	1220 CAGAATCCAT	1230 CGCCCTCAGT	1240 CACTGTTGCA	1250 TCAACCCCAT
1260 TATCTACTTG	1270 CTCTTCGGAC	1280 CTCGCTGTCTG	1290 AAGCGAGTTC	1300 TGTCACCTGT
1310 TGCGATGTTG	1320 CTTTACGCGC	1330 TTATGTCCAC	1340 ACAGATCCTG	1350 GAGTTCCATA
1360 CGTGCAGAGA	1370 CGGTGTCCAT	1380 CAGTCTCAGT	1390 CACTCACAGG	1400 TATCTGCATC
1410 ATCTGAGGAT	1420 GATGACAACG	1430 ATGTGCATGA	1440 TGAATTGCAA	1450 TTTTTAATTT
1460 GA -----				

FIG. 5B



10	20	30	40	50
ATGACCAATC	TTTACTCTGC	CAATTTTCTC	ACCTTGATAG	TACTTCCTTT
60	70	80	90	100
TATCGTTTTA	AGCAATCAAC	ACCTTTTACC	TGCCAGTGCA	GTAACCTGTA
110	120	130	140	150
AATTTCTCTC	CCTGTTGTAC	TACTCTAGCT	GCAGCGTAGG	TTTTGCTACA
160	170	180	190	200
GTGGCACTGA	TAGCGGCCGA	CCGATACCGA	GTGATTCATC	GCCGAACTCA
210	220	230	240	250
AGCTCGCCAA	TCCTACCGTA	ACACATATAT	GATAGTAGGC	TTAACGTGGC
260	270	280	290	300
TCATTGGCTT	GATCTGCGCT	ACCCCCGGGG	GGGTCTACAC	AACCATTGTA
310	320	330	340	350
GCTCACCGCG	ATGGGGAAAG	TGATGCTCAA	AGACACAATA	CTTGCAATTAT
360	370	380	390	400
GCACTTTGCG	TATGATGAAG	TTTACGTCCT	CATGGTCTGG	AAACTTCTCA
410	420	430	440	450
TCGTTTTAGT	CTGGGGCATA	GTGCCAGTTG	TCATGATGAG	CTGGTTTTAC
460	470	480	490	500
GCGTTTTTTT	ACAATACTGT	ACAAAGAACA	GCCAAAAAAC	AACAACGTAC
510	520	530	540	550
GTTGAAATTC	GTAAAGGTAT	TACTCCTGTC	ATTCATCATC	ATCCAAACTC
560	570	580	590	600
CCTATGTGTC	AATCATGATT	TTTAACACGT	ATGCCACCGT	AGGATGGCCG
610	620	630	640	650
ATGGAATGCG	CCGATCTAAC	TAGACGCCGA	GTCATCAACA	CGTTTTCCCG
660	670	680	690	700
TCTCGTCCCC	AATCTACATT	GCATGGTCAA	CCCCATCCTC	TACGCTCTCA
710	720	730	740	750
TGGGAAATGA	CTTTGTGTCT	AAAGTGGGCC	AATGCTTTTCG	GGGGGAACTC
760	770	780	790	800
ACGAACCGTC	GAACTTTTCT	GCGTTCCAAG	CAACAAGCCC	GCAACTCGGA
810	820	830	840	850
CGATGTACCG	ACAATTGTCA	GTCAACAACC	CGCCACACCC	ACCATCGTCA
860	870	880	890	900
ATAAGCCCGA	AAAAAACCCG	CACGTAAAC	GCGGTGTATC	TTTCAGCGTC
910	920	930	940	950
AGCGCATCTT	CCGAACTCGC	AGCGGCCAAA	AAAGCCAAAG	ACAAAGCCAA
960	970	980	990	
GCGGCTTTCC	ATGTCCCACC	AAAACCTACG	TCTGACGTGA	

FIG. 6



10	20	30	40	50
ATGGCAGTCA	CTTTACGAGG	CGGCAGCCCCG	ATAAACTTTA	AACTCATGAT
60	70	80	90	100
TGTCAGCCAC	AGAAACCGGA	AATTTTACGA	GATACGGCTG	TTTCAGCGTT
110	120	130	140	150
CTGCTATCCG	TCCAGGCGGG	TTATGGAAAC	CATTCTTCAC	AACCGAACG-
160	170	180	190	200
-----	-----	-----	-----	-----
210	220	230	240	250
-----	-----	---- AGTGA	AACTAATTCC	ATTTTGCACA
260	270	280	290	300
TCAACACCAC	CTGCAATGTG	ACCGACTCAC	TGTACGCCGC	CAAAC TAGGC
310	320	330	340	350
GAAGCCCTCG	TGAACAGCGC	GCTAGCTTTA	TTCGGTACCC	CCCTCAACGC
360	370	380	390	400
CATCGTCCTC	GTCACACAGC	TATTGGCCAA	CCGAGTTCAT	GGATACTCCA
410	420	430	440	450
CCCCGATTAT	CTACATGACC	AATCTTTACT	CTGCCAATTT	TCTCACCTTG
460	470	480	490	500
ATAGTACTTC	CTTTTATCGT	TTTAAGCAAT	CAACACCTTT	TACCTGCCAG
510	520	530	540	550
TGCAGTAACC	TGTAAATTTT	TCTCCCTGTT	GTACTACTCT	AGCTGCAGCG
560	570	580	590	600
TAGGTTTTGC	TACAGTGGCA	CTGATAGCGG	CCGACCGATA	CCGAGTGATT
610	620	630	640	650
CATCGCCGAA	CTCAAGCTCG	CCAATCCTAC	CGTAACACAT	ATATGATAGT
660	670	680	690	700
AGGCTTAACG	TGGCTCATTG	GCTTGATCTG	CGCTACCCCC	GGGGGGGTCT
710	720	730	740	750
ACACAACCAT	TGTAGCTCAC	CGCGATGGGG	AAAGTGATGC	TCAAAGACAC
760	770	780	790	800
AATACTTGCA	TTATGCACTT	TGCGTATGAT	GAAGTTTACG	TCCTCATGGT
810	820	830	840	850
CTGGAAACTT	CTCATCGTTT	TAGTCTGGGG	CATAGTGCCA	GTTGTCATGA
860	870	880	890	900
TGAGCTGGTT	TTACGCGTTT	TTTTACAATA	CTGTACAAAG	AACAGCCAAA
910	920	930	940	950
AAACAACAAC	GTACGTTGAA	ATTCGTAAAG	GTATTACTCC	TGTCATTTCAT
960	970	980	990	1000
CATCATCCAA	ACTCCCTATG	TGTCAATCAT	GATTTTTTAA	ACGTATGCCA

FIG. 7A



1010	1020	1030	1040	1050
CCGTAGGATG	GCCGATGGAA	TGCGCCGATC	TAAC TAGACG	CCGAGTCATC
1060	1070	1080	1090	1100
AACACGTTTT	CCCGTCTCGT	CCCCAATCTA	CATTGCATGG	TCAACCCCAT
1110	1120	1130	1140	1150
CCTCTACGCT	CTCATGGGAA	ATGACTTTGT	GTCTAAAGTG	GGCCAATGCT
1160	1170	1180	1190	1200
TTCGGGGGGA	ACTCACGAAC	CGTCGAACTT	TTCTGCGTTC	CAAGCAACAA
1210	1220	1230	1240	1250
GCCCGCAACT	CGGACGATGT	ACCGACAATT	GTCAGTCAAC	AACCCGCCAC
1260	1270	1280	1290	1300
ACCCACCATC	GTCAATAAGC	CCGAAAAAAA	CCCGCACGTA	AAACGCGGTG
1310	1320	1330	1340	1350
TATCTTTTCAG	CGTCAGCGCA	TCTTCCGAAC	TCGCAGCGGC	CAAAAAAGCC
1360	1370	1380	1390	1400
AAAGACAAAG	CCAAGCGGCT	TTCCATGTCC	CACCAAAACC	TACGTCTGAC
1410				
GTGA-----				

FIG. 7B



10 ATGATTACGG	20 AGCGCGTCCT	30 CGCAGGCATC	40 CTCGCGGGCA	50 TGACGGCCGC
60 GGGGAGTTTG	70 GTCATTCTCC	80 TCGCGGTTGT	90 TATGTGGTTG	100 AACATGTTAG
110 ATCGCGCTGG	120 CATGCCAATG	130 GCCGTTGGGC	140 ATTACACAGG	150 GAACCTGGTG
160 TTGACTCAGG	170 TCATCTGTAT	180 CTTCTCCATG	190 CTGGCGTCTA	200 AAATTGTTGG
210 CATGACGAGT	220 GCGGCCAACA	230 TGGGCTTCTG	240 CGGCATCGTG	250 GTTTTTCTGG
260 AAGACACTGG	270 CCTCTATGTC	280 ACCTCGCTGC	290 TCTTCATGTT	300 TATGATCCTG
310 GATCGCATGG	320 CGGCTTTTCT	330 TAACGGGCGT	340 CTTTTCTGGA	350 GGCAGCAGAC
360 GACGAAGCAG	370 AATCTGAGTA	380 CAAGCGTGTA	390 CATTATTCTG	400 TTTGTCTGGG
410 TGTTGGGAAT	420 GGCCGCGGCT	430 GTTCCCAGCG	440 CGGCTGTGGC	450 TGCACCCAAT
460 TCCAGGTGGG	470 AACGCTGCGA	480 AATTCCAGTG	490 TCATATGCCG	500 CAATCGACAT
510 GATTGTGAAG	520 CTCTGGTTTG	530 TGCTGTTGGC	540 ACCCGTCGTG	550 CTGATTATGG
560 CTGTGATCAT	570 TCAATCTTCC	580 TATCATCGTG	590 ATCGGGAGAG	600 GATCTGGTAC
610 TATGCCAGAC	620 GTGTGTTCAT	630 GTTCTACACG	640 GCCTGCTTTG	650 TCATGATGGT
660 GCCTTATTAC	670 TTCGTCAGAG	680 TCATGCTGAG	690 CGACTTTGCT	700 TTGGTTGATA
710 TAAAAACAAA	720 AACGGCGAAC	730 AGCGACGGTT	740 GTGATTCGAC	750 ATTTCTTGAT

FIG. 8A



760	770	780	790	800
TATCTGAACA	TGTTCACTCA	CGTGATTTAC	AGTTTTAAGT	TGGTGGTGTT
810	820	830	840	850
TGCTTTGTTC	ATTGTCCTGT	TTTGCTCCAT	AAACCCGATG	GAAACGCTGG
860	870	880	890	900
AAGAATGCTT	GGAGAGGGCC	GATGCTGAGA	GGCAAAGTCG	GTCAGAAGCA
910	920	930	940	950
TCCCAGGGTG	AAAGGAGGCT	GCCAATCAAC	ACATGCTGTA	TAAAGTTGAT
960	970	980	990	1000
TGAATTGATA	AAGCAGTATG	TAAGCACTCT	CTCTAAAGCC	ACGAGGGACA
1010	1020	1030	1040	1050
ATTCTGGCGA	AAGGGCCAAT	TTGCCAGAGA	ATGCTGAAGA	TATTGGAACA
1060	1070	1080	1090	1100
ACTGGCAGTG	ATCAGCTACC	GACTGAGGTC	ACCGTGACCC	CAAATTCATC
1110	1120	1130	1140	
GGCTGTGTTT	AGCACTGGAG	GAACGGTGTC	TCCAGTCTAA	

FIG. 8 B



Annotated Sheet Showing Changes

~~Rh0328.4~~

AT

10	20	30	40	50	60
GAATTCGAGC	CAGCACAACA	TAAGCGTGTT	TCTCTCCATT	GGAGCAGGGC	CCGTCATTAC
70	80	90	100	110	120
CGGATACACG	TGCGTTTTTC	TGTTCCGGAT	TCTGGGACAC	TTTACTTGT	ATTGGAAAAA
130	140	150	160	170	180
CCATCAGAGA	CGACACCGGA	CAAACAGTTT	CAGTGATGTT	TTATTTTCGAC	ATCTCATGAT
190	200	210	220	230	240
CACCGAAGAG	GTCTTTACCC	TCACCATTC	CGTCTGGGCG	TATCACTTAA	CTACTCACGG
250	260	270	280	290	300
CAACTTACCG	GGCTCGTGGT	GCCGAAGTCT	CACCTTCGTT	TTTTATCTAA	CGGTATTTCG
310	320	330	340	350	360
TCGTGCCCTT	TTTTACCTGC	TCCTCATCTG	GGACCGATAC	AGCGTAATCA	TCTGCAGACA
370	380	390	400	410	420
CCCTCTCCCC	GTAAATCTGA	ACTACAGTCA	GGTCATAGGC	CTGTCTGTCT	GGCTGGTTGC
430	440	450	460	470	480
CGTACTGTCA	GCATCACCGT	TCTCCATTTT	TAACGGAAGT	GTGAAACAAT	GCCTGGGCAA
490	500	510	520	530	540
CATGGGCAGC	ATACCCAGCG	AATCGTCTGC	CGTTCTTAAC	CTGGAAGTGC	ACCTGTGCTC
550	560	570	580	590	600
CTTCTGGTTA	CCGCTCATCA	TGTCGGCTAA	CTGTTACTAC	CAAGCAAAAC	GCCGAGCATC
610	620	630	640	650	660
GCCTGACCAA	CTCCACGAAC	TTTACCGATG	CAGTTTGCTA	ATTACCAFTA	TCACAACFTA
670	680	690	700	710	720
CGCTATCGTA	TGGTTTCCTT	TCCATCTCGC	TTTACTCATA	GACGCCCTGA	TTAGCATAAG
730	740	750	760	770	780
CCATGTAGAA	CCCTCTAGCG	CTCTCCACTG	GGCATCCATT	GTCGTTACCT	GTAAATCATT
790	800	810	820	830	840
TACAFTTGTA	TATGCGGGCA	TAAGCCCACT	AGTGTATTTT	ACATGCTGCC	CCACCGTACG
850	860	870	880	890	900
TCGCGAAGTG	CTGATGTCTC	TACGTCCATT	CTTCACCTGG	ATTTCCAGCA	AAACGCGGCG
910	920	930	940	950	960
AGGCTACGCT	CCGATTAAAA	CACAACCTTT	AAACATCCCC	GACGAGCCGA	TAGATAACAA
970	980	990	1000	1010	1020
GTCACCGCAC	CTGTAAACG	AATAA.....